AMENDMENTS TO AND LISTING OF THE CLAIMS

Please cancel claims 25-27 and 40-150 without prejudice.

Please amend claims 2, 3, 5, 19 and 24 as follows:

1. (Original) A method for selecting a crossover location in a first biopolymer having a first polymer sequence, for recombination with one or more second biopolymers each having its own second polymer sequence, which method comprises:

identifying coupling interactions between pairs of residues in the first polymer sequence;

generating a plurality of data structures, each data structure representing a crossover mutant comprising a recombination of the first and a second polymer sequence wherein each recombination has a different crossover location;

determining, for each data structure, a crossover disruption related to the number of coupling interactions disrupted in the crossover mutant represented by the data structure; and

identifying, among the plurality of data structures, a particular data structure having a crossover disruption below a threshold,

wherein the crossover location of the crossover mutant represented by the particular data structure is the identified crossover location.

2. (Currently Amended) A method of claim 1, wherein the ~~particular~~ first polymer sequence comprises a sequence of amino acid residues.

3. (Currently Amended) A method of claim 1, wherein the ~~particular~~ first polymer sequence comprises a sequence of nucleotide residues.

4. (Original) A method of claim 1, wherein coupling interactions are identified by use of a coupling matrix.

5. (Currently Amended) A method of claim [[1]] 4, wherein the coupling matrix is the summation of all the coupling interactions of the first polymer sequence.

6. (Original) A method of claim 1, wherein coupling interactions are identified by a determination of a conformational energy between residues.

7. (Original) A method of claim 1, wherein coupling interactions are identified by a determination of interatomic distances between residues.

8. (Original) A method of claim 6, wherein conformational energies for each of the first and second polymer sequences are determined from a three-dimensional structure for at least one of the first and second polymer sequences.

9. (Original) A method of claim 7, wherein interatomic distances for each of the first and second polymer sequences are determined from a three-dimensional structure for at least one of the first and second polymer sequences.

10. (Original) A method of claim 2, wherein coupling interactions are identified by a conformational energy between residues above a threshold.

11. (Original) A method of claim 1, wherein a coupling interaction between a pair of residues in the first polymer sequence is disrupted in a crossover mutant wherein a coupling interaction between a pair of residues is disrupted in a crossover mutant if the identity of both residues participating in the coupling interaction is different than that which exists in any of the parents.

12. (Original) A method of claim 8, wherein a coupling interaction between a pair of residues in the first polymer sequence is disrupted in a crossover mutant wherein a coupling interaction between a pair of residues is disrupted in a crossover mutant if the identity of both residues participating in the coupling interaction is different than that which exists in any of the parents.

13. (Original) A method of claim 1, wherein the crossover disruption is the summation of all coupled interactions in the parent that are considered disrupted in the data structure representing the crossover mutant.

14. (Original) A method of claim 1, wherein the threshold is an average level of crossover disruption for the plurality of data structures.

15. (Original) A method of claim 1, wherein the threshold is at least one standard deviation below the average level for the plurality of data structures.

16. (Original) A method of claim 1, wherein the threshold is set so that approximately 7.5% of the total number of generated data structures is below the threshold.

17. (Original) A method of claim 1, wherein the threshold is set so that approximately 1% of the total number of generated data structures is below the threshold.

18. (Original) A method of claim 1, wherein the threshold is set so that approximately 0.001% of the total number of generated data structures is below the threshold.

19. (Currently Amended) A method of claim 1, wherein the generation of crossover mutants comprises:

the sequence alignment of a plurality of biopolymers;

the identification of possible cut points in the plurality of biopolymers ~~biopolymer~~ based upon regions of sequence identity identified by the sequence alignment; and

the generation of single crossover mutants based upon the identified possible cut points.

20. (Original) A method of claim 19, wherein the regions of sequence identity must contain at least 4 residues.

21. (Original) A method of claim 19, there must be at least eight residues between crossovers.

22. (Original) A method of claim 1, wherein the generation of the plurality of data structures comprises:

the sequence alignment of a plurality of biopolymers using simulated annealing with non-homologous parents;

selecting crossover locations based upon the minimization of crossover disruption, fragment size, starting number of parents; and

the generation of a plurality of data structures based upon the identified possible crossover locations.

23. (Original) A method of claim 1, wherein the generation of the plurality of data structures comprises:

choosing one of the biopolymers from the plurality of biopolymers at random;

copying the biopolymer until a possible crossover location is reached;

choosing a random number between 0 and 1;

choosing a new biopolymer from the plurality of biopolymers to copy to the offspring if the random number is below a crossover probability (Pc); and

repeating the above process until the data structure representing the crossover mutant is the desired length.

24. (Currently Amended) A method of claim 19, wherein the generation of the plurality of data structures based upon identified cut points comprises:

cutting the biopolymers in into biopolymer fragments by randomly assigning cut points with a set probability;

randomly choosing one of the biopolymer fragments as a starting parent;

randomly identifying another biopolymer fragment from the total pool of the biopolymer fragments;

ligating the identified biopolymer fragment to the parent fragment, if the identified biopolymer fragment has [[a]] an ~~sequence identity~~ identified possible cut-point at the end of the fragment; and

repeating the randomly identifying step and the ligating step until the data structure~~, representing the crossover mutant~~ is the desired length.

Claim 25-27. Canceled without prejudice

28. (Original) A computer system for analyzing a polymer sequence, which computer system comprises:

memory and a processor interconnected with the memory and having one or more software components loaded therein, wherein the one or more software components cause the processor to execute steps of a method according to claim 1.

29. (Original) A computer system of claim 28, wherein the software components comprise a database of polymer sequences.

30. (Original) A computer system of claim 28, wherein the software components comprise a database of three-dimensional structures for polymer sequences.

31. (Original) A computer program comprising a computer readable medium having one or more software components encoded in computer readable form, wherein the one or more software components may be loaded into a memory of a computer system and cause a processor interconnected with the memory to execute steps of a method according to claim 1.

32. (Original) A computer program according to claim 30, wherein the computer readable medium further has, encoded thereon in computer readable form, a database of polymer sequences.

33. (Original) A computer program according to claim 30, wherein the computer readable medium further has, encoded thereon in computer readable form, a database of three-dimensional structures for polymer sequences.

34. (Original) A computer system for analyzing a polymer sequence, which computer system comprises:

memory and a processor interconnected with the memory and having one or more software components loaded therein, wherein the one or more software components cause the processor to execute steps of a method according to claim 19.

35. (Original) A computer program comprising a computer readable medium having one or more software components encoded in computer readable form, wherein the one or more software components may be loaded into a memory of a computer system and cause a processor interconnected with the memory to execute steps of a method according to claim 19.

36. (Original) A computer system for analyzing a polymer sequence, which computer system comprises:

memory and a processor interconnected with the memory and having one or more software components loaded therein, wherein the one or more software components cause the processor to execute steps of a method according to claim 23.

37. (Original) A computer program comprising a computer readable medium having one or more software components encoded in computer readable form, wherein the one or more software components may be loaded into a memory of a computer system and cause a processor interconnected with the memory to execute steps of a method according to claim 23.

38. (Original) A computer system for analyzing a polymer sequence, which computer system comprises:

memory and a processor interconnected with the memory and having one or more software components loaded therein, wherein the one or more software components cause the processor to execute steps of a method according to claim 24.

39. (Original) A computer program comprising a computer readable medium having one or more software components encoded in computer readable form, wherein the one or more software components may be loaded into a memory of a computer system and cause a processor interconnected with the memory to execute steps of a method according to claim 24.

Claims 40-150. Canceled without prejudice.

151. (Original) A method of claim 1, wherein a coupling interaction between a pair of residues in the first polymer sequence is disrupted in a crossover mutant if the identity of a residue is different in the crossover mutant than in the first polymer sequence, and wherein a coupling interaction between a pair of residues is scaled by the probabilities that the identity and sequence position of the coupled residues are the same in both parents.

* * * * *